

FIGURE 1

rpoB gene of *M. tuberculosis*

Total: 531 bp

tca aggaagaaagc ctacgaactg gcccgcgctcg gtcgctataa (43)
 ggtcaacaag aagctcgggc tgcattgtcgg cgagcccatc acgtcgtcga cgctgaccca (103)
 agaagacgtc gtggccacca tgaatatctt ggtccgcttg cagcagggtc agaccacgat (163)
 gaccgttcgg ggcggcgctcg aggtgcgggt ggaaccggac gacatcgacc acttcggcaa (223)
 ccgcgcgtctg cgtacgggtcg tggagctgat ccaaaaccag atccgggtcg gcatgtcggc (283)
 gatggagcgg gtggtccggg aggggtgac caccacggac gtggagggca tcaacaccca (343)
 gacgttgatc aacatccggc cgtgtgtcgc cggcatcaag gattcttcg gccacaccca (403)
 gctgagccaa ttcattggacc agaacacccc gctgtcgggg ttgacccaca agcgcgcgact (463)
 gtcgggcctg gggcccgagg gtctgctcgt tggcgctgc ggtctggggg tccggcgacgt (523)
 gccacccgt

Underlined letters: Primer binding regions

Bold Letters: polymorphic region existing in *M. tuberculosis* and MOTTs

Italic letters: the region related to the resistance against rifampin

FIGURE 2

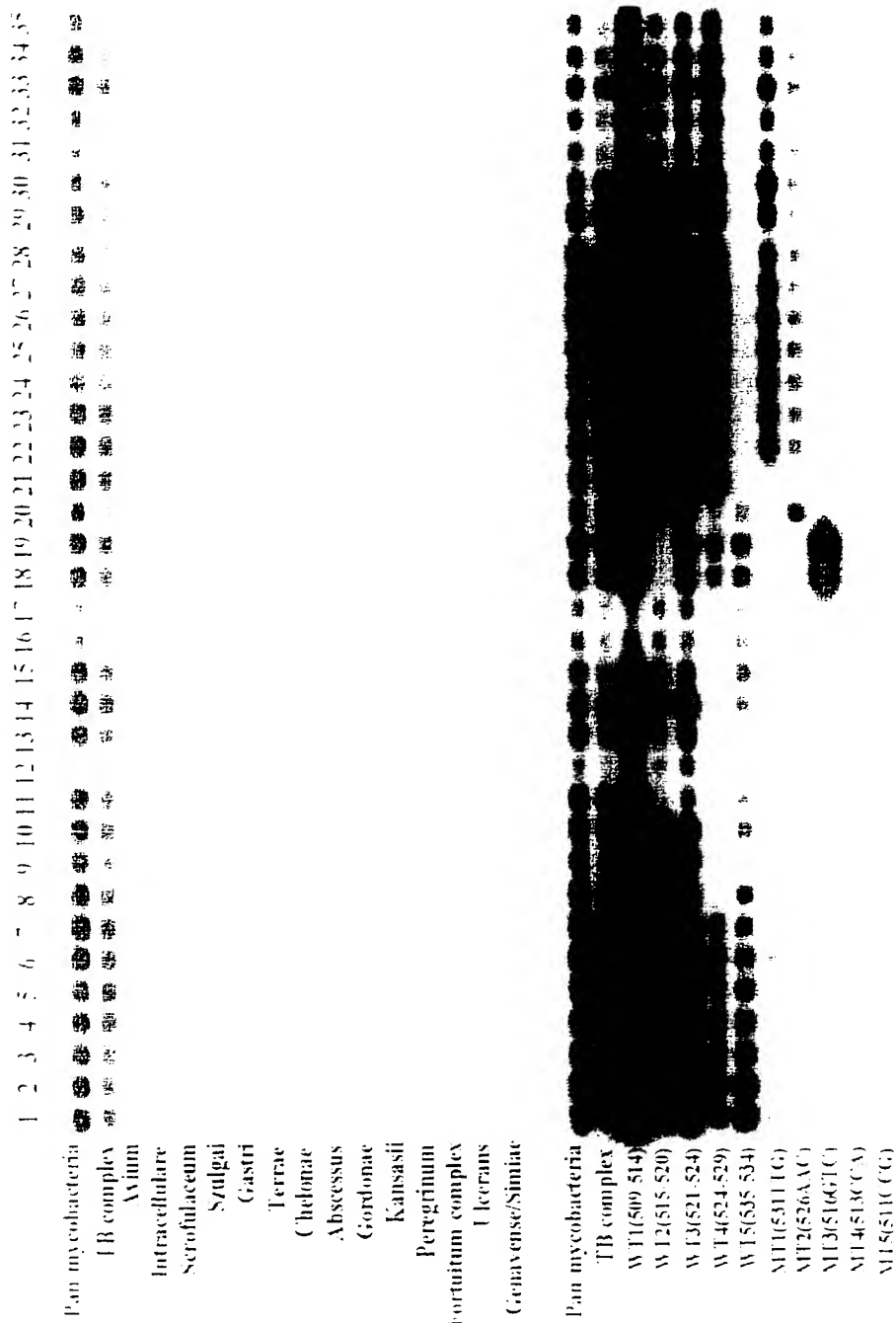


FIGURE 3

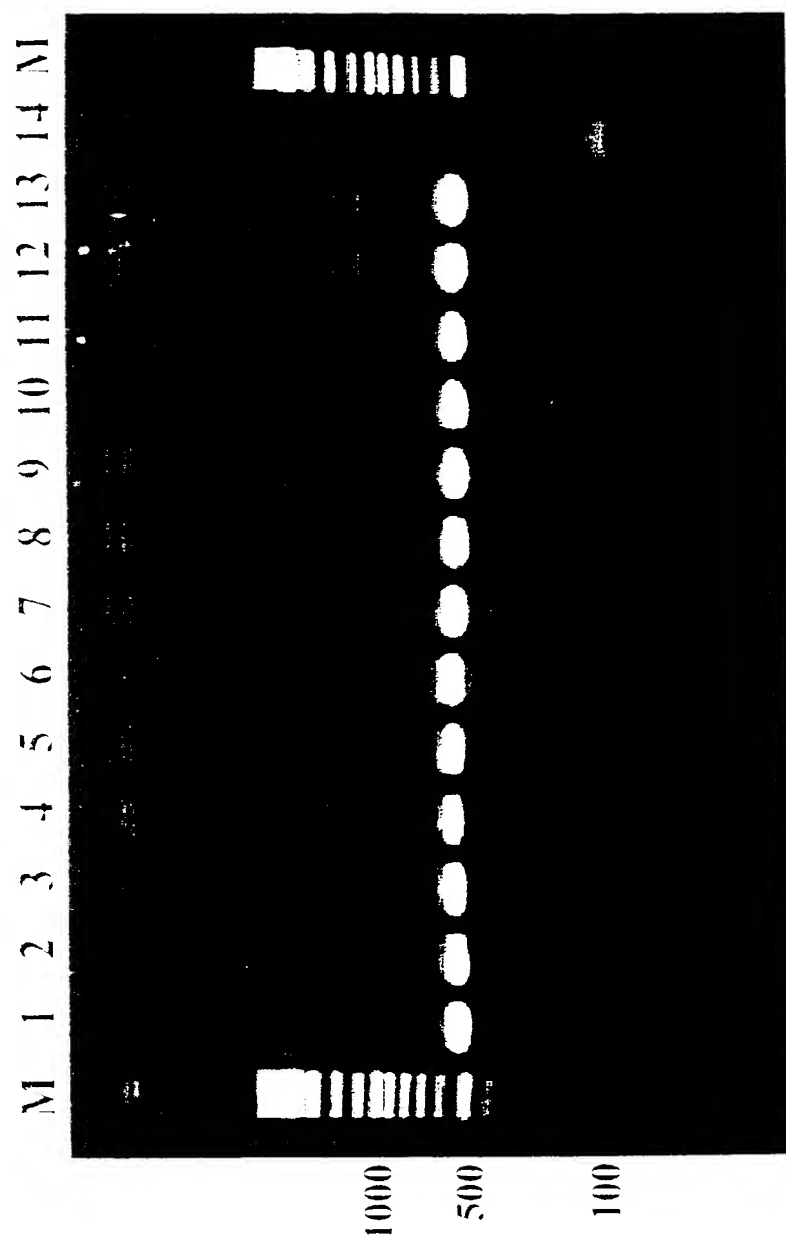


FIGURE 4

M. phylum
M. terminatum
M. caecale
M. riviale
M. hominis
M. phlei
M. paratuberculosis
M. flavescens
M. malmoense
M. celatum II
M. celatum I
M. neo-chromogenicum
M. simiae
M. genavense
M. marinum
M. ulcerans
M. peregrinum
M. fortuitum II
M. fortuitum I
M. kansasii
M. goodii
M. abscessus
M. mageritensis
M. terrae
M. gastri
M. szulgai
M. scrofulaceum
M. intracellulare
M. avium
M. microti
M. africanum
M. bovis B67
M. bovis
M. tuberculosis H37Rv

Pan-mycobacteria
 TB complex
 Avium
 Intracellular
 Scrofulaceum
 Szulgai
 Gastri
 Terrae
 Chelonae
 Abscessus
 Goodii
 Kansasii
 Peregrinum
 Fortuitum complex
 Ulcerans
 Genavense/Simiae

FIGURE 5

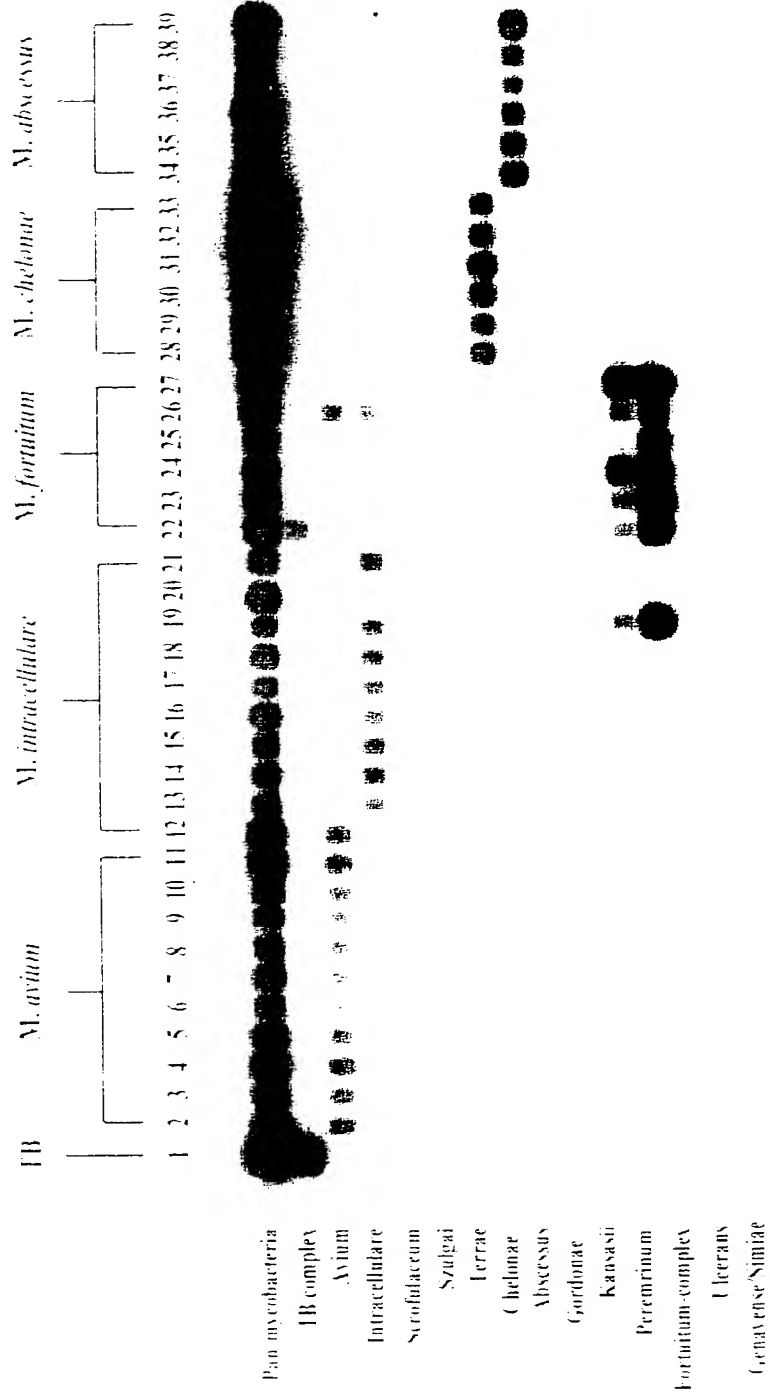


FIGURE 6

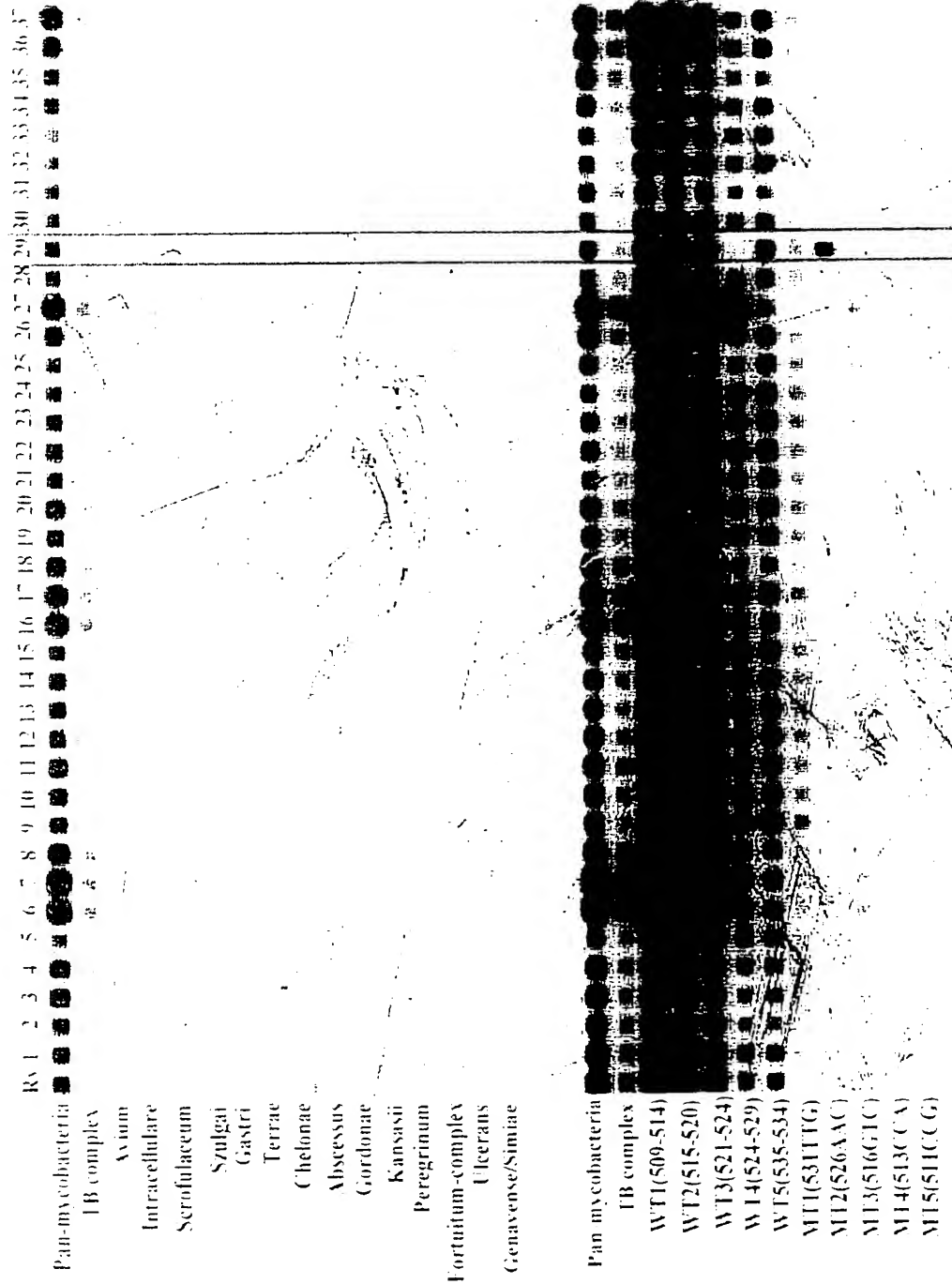


FIGURE 7